MOLECULAR CHARACTERIZATION AND ANTIBIOTIC SUSCEPTIBILITY PATTERN OF *Staphylococcus aureus* ISOLATED FROM CLINICAL AND ENVIRONMENTAL SOURCES

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ABSTRACT

Staphylococcus aureus is an important pathogen causing skin and soft-tissue infections, systemic infections and toxemic syndromes. In order to have adequate information for treatment of *S.aureus* infections, it is important to understand trends in the antibiotic-resistance patterns as well as clonal identities across geographical regions. A total of 297 non-duplicate *S. aureus* isolates (209 clinical, 84 carrier and 4 environmental) were characterized by phenotypic and genomic methods. Antimicrobial susceptibility testing was performed by disk diffusion and the automated VITEK-2 system. PCR was used to amplify genes for accessory gene regulator (*agr*); capsular polysaccharide (*cap*) 5 and 8, exfoliative toxins (*eta* and *etb*), the toxic shock syndrome toxin-1(*tst*) and Panton-Valentine Leukocidin (PVL). Typing of isolates was by the staphylococcal protein A (*spa)* typing. High level resistance was observed against penicillin and ampicillin (97.3%); trimethoprim/sulfamethoxazole (80%) and tetracycline (17.5%). Azithromycin, clarithromycin, erythromycin, clindamycin, linezolid, vancomycin, nitrofurantoin, fusidic acid, mupirocin and rifampicin recorded 100% activity against the isolates. Ninety-five percent of all strains (n=281) harboured the β-lactamase (*blaZ*) gene and 2.7% (n=8) possessed the *mecA* gene. The methicillin resistant *S. aureus* (MRSA) strains were resistant to at least 10 antibiotics including all penicillins, penicillin/penicillinase inhibitor combinations, carbapenem and cephalosporins. The staphylococcal cassette chromosome *mec* (SCC*mec*) typing of MRSA strains detected only SCC*mec* types I and IV in two strains (Y260: type I and Y59: type IV). The *eta* and *tst* genes were present in 0.7% (n=2) and 1.7% (n=5) of *S. aureus* isolates respectively. A high prevalence of PVL genes was noted in clinical isolates (79.4%; n=166); carrier isolates (56%; n=47) and environmental isolates (75%; n=3). The PVL protein was expressed *in vitro* by 68.5% of strains harboring *lukS-PV* and *lukF-PV* gene. All strains carried either the *cap8* (91.9%; n=273) or *cap5* locus (7.7%; n=23) while one MRSA strain was untypeable. A Single *agr* allele was detected in each *S. aureus* isolate with the majority in *agr-2* (73.4%; n=218). Thirty-seven *spa* types were identified; predominant *spa* types among the methicillin-susceptible *S. aureus* (MSSA) were t084 (65%), t2304 (4.4%) and t8435 (4%). Prevalent *spa* types in MRSA were t002, t008, t064, t194, t8439, t8440 and t8441. Eleven novel *spa* types (t8435, t8436, t8437, t8438, t8439, t8440, t8441, t8442, t8952, t8953, t8953) were identified. The pT181 plasmid was successfully used to confer tetracycline resistance in *S. aureus* strains A56 and Y1. The use of phenotypic and molecular methods in this study provided useful information on antibiotic resistance and genetic diversity of *S. aureus* isolates from Ogun and Lagos States of Nigeria.

The information provided could help in monitoring the evolution of *S. aureus* strains in Nigeria over
time.